

SEQUENCE LISTING

<110> De Sauvage, Frederic J.
Klein, Richard D.
Rosenthal, Arnon
Phillips, Heidi S.

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<212> DNA

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<211> 397

<212> PRT

<213> Mus musculus

<400> 6

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Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
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Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
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Asn	Asp	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	
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Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Val	Glu	His	Ile	Pro
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Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	Ser
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Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg
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Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe
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Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile
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Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	Asn	Glu	Ile	Pro	Thr
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His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu	Lys	Ser
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Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	Asn	Gly	Asn	Tyr	Glu
				405					410					415	
Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	Thr	Lys	Ser	Met	Ala
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 <212> PRT
 <213> Homo sapiens

<400> 7

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Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys
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Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	Ser	Ile
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Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	Lys	Lys
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Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	Pro	Thr
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Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe
			195				200					205			
Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
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Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser
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Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Gly
				245				250						255	
Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
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Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Pro	Thr	Gly	Ile	Val	Val	Ser
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Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
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Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
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Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
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 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
 385 390 395 400
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 405 410 415
 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
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<210> 8
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 <213> Rattus norvegicus

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 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
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 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
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 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
 225 230 235 240
 Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
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385		390		395
Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser				
	405		410	415
Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile				
	420		425	430
Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu				
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<210> 9
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 <213> Rattus Norvegicus

<400> 9
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35 40 45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
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Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65 70 75 80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
100 105 110
His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
115 120 125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
130 135 140
Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His
145 150 155 160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
165 170 175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
180 185 190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Glu Phe Phe
195 200 205

Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
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225					230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser
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Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
			260					265					270		
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala	Asp
	275						280					285			
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	290					295					300				
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val	Ser
305					310					315					320
Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
			325						330						335
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
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Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly	Pro
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Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
	370					375					380				
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
385					390					395					400
Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
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Ser	Lys	Lys	Val	Ile	Lys	Leu	Asn	Ser	Gly	Ser	Ser	Arg	Ala	Arg	Leu
	435						440					445			
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 <213> Homo sapiens

<220>

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atgaacagct gtctccaggc caggaggaag tgccaggctg atcccacctg cagtgtctgcc 180
taccaccacc tggattcctg cacctctagc ataagcacc cactgccctc agaggagcct 240
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tgcatgtgcc accggcgcat gaagaaccag gttgcctgct tggacatcta ttggaccgtt 360
caccgtgccc gcagccttgg taactatgag ctggatgtct cccctatga agacacagt 420
accagcaaac cctggaaaat gaatctcagc aaactgaaca tgctcaaacc agactcagac 480
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tgtgcaacag agcagtcag atgtctacga gcataacctg ggctgattgg gactgccatg 900
acccccaaact ttgtcagcaa tgtcaacacc agtgttgct taagctgcac ctgcccaggc 960
agtggcaacc tgcaggagga gtgtgaaatg ctggaagggt tcttctccca caacccctgc 1020
ctcacggagg ccattgcagc taagatgcgt ttccacagcc aactcttctc ccaggactgg 1080
ccacacccta cctttgctgt gatggcacac cagaatgaaa accctgctgt gaggccacag 1140
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tagctggact tccccagggc cctcttcccc tccaccacac ccagggtggac ttgcagccca 1260
caaggggtga ggaaaggaca gcagcaggaa ggagggtgag tgcgcagatg agggcacagg 1320
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atctccactt ctgattcatg ctgcccctcc ttggtggcca caatttagcc atgtcatctg 1440
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agaatctaata agtttagcct ttctctattg cattccagat taggggttagg gtagggagga 1560
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tcgtctctct ctctgagtgg aggatggaaa actactgcct gcactgccct gtccccggat 1680
cctgccgaac atctgggcat caggagctgg agcctgtggg ccttgcttta ttctattat 1740
tgtctaaag tctctctggg ctcttgatc atgattaaac ctttgactta ag 1792

<210> 15

<211> 400
 <212> PRT
 <213> Homo Sapiens

<400> 15

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
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Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25					30		
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35					40					45			
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
	50					55					60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70					75					80
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85					90					95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
		115				120						125			
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145					150					155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
				165					170					175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
	195					200						205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
	210					215					220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	
225					230				235					240	
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
				245					250					255	
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
			260					265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
	275					280						285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
	290					295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
				325					330					335	
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340					345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
		355					360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370					375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
385					390					395					400

<210> 16
 <211> 1837
 <212> DNA
 <213> Homo sapeins

<400> 16
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 gcccggcgcc tacagctcgc catggtgcgc cccctgaacc cgcgaccgct gccgccccta 180
 gtccctgatgt tgetgctgct gctgcccgcg tcgcccgtgc ctctcgagc cggagacccc 240
 cttccacacag aaagccgact catgaacagc tgtctccagg ccaggaggaa gtgccaggct 300
 gatccacact gcagtgtgct ctaccaccac ctggattcct gcacctctag cataagcacc 360
 ccaactgccct cagaggagcc ttccggtccct gctgactgcc tggaggcagc acagcaactc 420
 aggaacagct ctctgatagg ctgcatgtgc caccggcgca tgaagaacca ggttgccctgc 480
 ttggacatct attggaccgt tcaccgtgct cgcagccttg actcagacct ctgcctcaag 540
 tttgccatgc tgtgtactct caatgacaag tgtgaccggc tgcgcaaggc ctacggggag 600
 gcgtgctccg gggcccactg ccagcgccac gtctgacctca ggcagctgct cactttcttc 660
 gagaaggccg ccgagcccca cgcgaggggc ctgctactgt gccatgtgc cccaacgac 720
 cggggctgctg gggagcgccg gcgcaacacc atcgccccca actgcgcgct gccgctgtg 780
 gcccccaact gcctggagct gcggcgccctc tgcttctccg acccgctttg cagatcacgc 840
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 cagtccagat gtctacgagc atacctgggg ctgattggga ctgccatgac cccaacttt 960
 gtcagcaatg tcaacaccag tgttgcccta agctgcacct gccgaggcag tggcaacctg 1020
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 attgcagcta agatgcgttt tcacagccaa ctcttctccc aggactggcc acaccctacc 1140
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 tctcttttct cctgcacgct tcccttgatt ctgctcctga gcctatggta gctggacttc 1260
 cccaggggccc tcttcccctc caccacaccc aggtggactt gcagcccaca aggggtgagg 1320
 aaaggacagc agcaggaagg aggtgcagtg cgcagatgag ggcacaggag aagctaaggg 1380
 ttatgacctc cagatcctta ctggtccagt cctcattccc tccaccccat ctccacttct 1440
 gattcatgct gcccctcctt ggtggccaca atttagccat gtcattctgg ggtgaccagc 1500
 tccaccaagc ccctttctga gcccttctctc ttgactacca ggatcaccag aatctaataa 1560
 gttagccttt ctctattgca ttccagatta ggggttagggg agggaggact ggggtgttctg 1620
 aggcagccta gaaagtcatt ctcccttctg aagaaggctc ctgccccctc gtctcctcct 1680
 ctgagtgagg gatggaaaac tactgcctgc actgccctgt ccccgatcc tgccgaacat 1740
 ctgggcatca ggagctggag cctgtgggccc ttgctttatt cctattattg tcctaaagtc 1800
 tctctgggct cttggatcat gattaaacct ttgactt 1837

<210> 17
 <211> 369
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95
 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala

				85					90					95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
		115					120					125			
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145					150					155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
			165					170						175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
	195					200						205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
	210					215					220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
225					230					235					240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
			245					250						255	
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
		260						265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
	275						280					285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
	290					295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
			325					330						335	
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
		340						345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
	355					360						365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370					375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
385					390					395					400
Pro	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
			405					410						415	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
		420						425					430		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
	435					440						445			
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	450					455					460				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
465					470					475					480
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
			485					490						495	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
		500						505					510		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
	515						520					525			
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
	530					535					540				

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 545 550 555 560
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Tyr Lys Thr Thr Pro
 565 570 575
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 580 585 590
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 595 600 605
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 610 615 620
 Ser Pro Gly Lys
 625

<210> 19
 <211> 951
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric receptor comprising rat sequence.

<400> 19
 Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
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 Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20 25 30
 Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45
 Val Leu Asp Gln Leu Leu Glu Pro Ser Ser Leu Gln Gly Ser Glu Leu
 50 55 60
 His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys
 65 70 75 80
 Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys
 85 90 95
 Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln
 100 105 110
 Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys
 115 120 125
 Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser
 130 135 140
 Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro
 145 150 155 160
 Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser
 165 170 175
 Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn
 180 185 190
 His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys
 195 200 205
 Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro
 210 215 220
 Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
 225 230 235 240
 Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser
 245 250 255
 Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro
 260 265 270

Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg
		275					280					285			
Ser	Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe
	290					295					300				
His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala
305					310					315					320
Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe
			325						330					335	
Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val
			340						345				350		
Ser	Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys
		355					360					365			
Glu	Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala
	370					375					380				
Ile	Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly
385					390					395					400
Pro	Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser
				405					410					415	
Leu	Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile
			420					425					430		
Thr	Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser
		435					440					445			
Lys	Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro
	450					455					460				
Gly	Trp	Arg	Ala	Trp	Val	Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu
465					470					475					480
Val	Thr	Ala	Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys
				485					490					495	
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	Glu
			500					505					510		
Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	Arg	Glu	Arg	Pro
		515					520					525			
Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu
	530					535					540				
Lys	Glu	Lys	Leu	Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu
545					550					555					560
Gly	Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln
				565					570					575	
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	Lys	Met	Leu
			580					585					590		
Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu
		595					600					605			
Ala	Ala	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val
	610					615					620				
Gly	Val	Ser													

Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln
			740					745					750		
Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg
		755					760					765			
Gly	Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr
	770					775					780				
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	Met	Glu	Asp
785					790					795					800
Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg
				805					810					815	
Pro	Ser	Phe	Thr	Cys	Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln
			820					825					830		
Leu	Ser	Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu
		835					840					845			
Arg	Ala	Glu	Glu	Pro	Thr	Ala	Gly	Gly	Ser	Leu	Glu	Leu	Pro	Gly	Arg
	850					855					860				
Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	Gly	Ser	Gly	Met	Gly	Ala	Val
865					870					875					880
Gly	Gly	Thr	Pro	Ser	Asp	Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu
				885					890					895	
Ala	Glu	Gln	Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn
			900					905					910		
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His	Ser
		915					920					925			
Ser	Cys	Ala	Asp	Ala	Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg
	930					935					940				
Gly	Lys	Asp	Leu	Pro	Val	Leu									
945						950									

<210> 20

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor comprising murine sequence.

<400> 20

Met	Gly	Gly	Thr	Ala	Ala	Arg	Leu	Gly	Ala	Val	Ile	Leu	Phe	Val	Val
1				5					10					15	
Ile	Val	Gly	Leu	His	Gly	Val	Arg	Gly	Lys	Tyr	Ala	Leu	Ala	Asp	Ala
			20					25					30		
Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	Lys	Asp	Leu	Pro
		35					40					45			
Val	Leu	Asp	Gln	Leu	Leu	Glu	Ala	Gly	Asn	Ser	Leu	Ala	Thr	Glu	Asn
	50					55					60				
Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys	Glu	Ala	Asn
65					70					75					80
Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Gly	Ser	Cys	Thr	Ser	Ser
				85					90					95	
Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser	Ala	Asp	Cys
			100					105					110		
Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Asp	Cys	Arg
		115					120					125			
Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp	Ile	Tyr	Trp

130	135	140
Thr Val His Pro Ala Arg Ser Leu Gly Asp Tyr Glu Leu Asp Val Ser		
145	150	155
Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser		160
	165	170
Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala		175
	180	185
Met Leu Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr		190
	195	200
Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala		205
	210	215
Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His Ala Gln Gly		220
225	230	235
Leu Leu Leu Cys Pro Cys Pro Pro Glu Asp Ala Gly Cys Gly Glu Arg		240
	245	250
Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Thr Pro		255
	260	265
Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro Leu Cys Arg		270
	275	280
Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met Asp Ile Leu		285
	290	295
Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly		300
305	310	315
Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys Val Asn Thr		320
	325	330
Thr Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu Gln Asp		335
	340	345
Glu Cys Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro Cys Leu Val		350
	355	360
Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln		365
	370	375
Asp Trp Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln Asn Ser Asn		380
385	390	395
Pro Ala Trp Arg Ala Trp Val Pro Val Val Leu Gly Val Leu Thr Ala		400
	405	410
Leu Val Thr Ala Ala Ala Leu Ala Leu Ile Leu Leu Arg Lys Arg Arg		415
	420	425
Lys Glu Thr Arg Phe Gly Gln Ala Phe Asp Ser Val Met Ala Arg Gly		430
	435	440
Glu Pro Ala Val His Phe Arg Ala Ala Arg Ser Phe Asn Arg Glu Arg		445
	450	455
Pro Glu Arg Ile Glu Ala Thr Leu Asp Ser Leu Gly Ile Ser Asp Glu		460
465	470	475
Leu Lys Glu Lys Leu Glu Asp Val Leu Ile Pro Glu Gln Gln Phe Thr		480
	485	490
Leu Gly Arg Met Leu Gly Lys Gly Glu Phe Gly Ser Val Arg Glu Ala		495
	500	505
Gln Leu Lys Gln Glu Asp Gly Ser Phe Val Lys Val Ala Val Lys Met		510
	515	520
Leu Lys Ala Asp Ile Ile Ala Ser Ser Asp Ile Glu Glu Phe Leu Arg		525
	530	535
Glu Ala Ala Cys Met Lys Glu Phe Asp His Pro His Val Ala Lys Leu		540
545	550	555
Val Gly Val Ser Leu Arg Ser Arg Ala Lys Gly Arg Leu Pro Ile Pro		560
	565	570
Met Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ala Phe Leu		575
	580	585
		590

Leu Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln Thr
 595 600 605
 Leu Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr Leu Ser
 610 615 620
 Ser Arg Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu
 625 630 635 640
 Ala Glu Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Arg Lys
 645 650 655
 Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Cys Ala Ser Lys Leu Pro
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 Val Lys Trp Leu Ala Leu Glu Ser Leu Ala Asp Asn Leu Tyr Thr Val
 675 680 685
 Gln Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Met Thr
 690 695 700
 Arg Gly Gln Thr Pro Tyr Ala Gly Ile Glu Asn Ala Glu Ile Tyr Asn
 705 710 715 720
 Tyr Leu Ile Gly Gly Asn Arg Leu Lys Gln Pro Pro Glu Cys Met Glu
 725 730 735
 Asp Val Tyr Asp Leu Met Tyr Gln Cys Trp Ser Ala Asp Pro Lys Gln
 740 745 750
 Arg Pro Ser Phe Thr Cys Leu Arg Met Glu Leu Glu Asn Ile Leu Gly
 755 760 765
 Gln Leu Ser Val Leu Ser Ala Ser Gln Asp Pro Leu Tyr Ile Asn Ile
 770 775 780
 Glu Arg Ala Glu Glu Pro Thr Ala Gly Gly Ser Leu Glu Leu Pro Gly
 785 790 795 800
 Arg Asp Gln Pro Tyr Ser Gly Ala Gly Asp Gly Ser Gly Met Gly Ala
 805 810 815
 Val Gly Gly Thr Pro Ser Asp Cys Arg Tyr Ile Leu Thr Pro Gly Gly
 820 825 830
 Leu Ala Glu Gln Pro Gly Gln Ala Glu His Gln Pro Glu Ser Pro Leu
 835 840 845
 Asn Glu Thr Gln Arg Leu Leu Leu Gln Gln Gly Leu Leu Pro His
 850 855 860
 Ser Ser Cys Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg Phe
 865 870 875 880
 Arg Gly Lys Asp Leu Pro Val Leu
 885

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 <213> Homo sapiens

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37

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<400> 23
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